

Figure 1

SEQ ID NO: 21	(gi 1709203)	1	MARNGSLEEF	60
SEQ ID NO: 22	(gi 1709205)		MAQNGSVEQ	
SEQ ID NO: 2			MAE-----EQFLAVAVDA	
SEQ ID NO: 4			MVDNDSLSE	
SEQ ID NO: 6			MAE-----EQFLAAAVGA	
SEQ ID NO: 8				
SEQ ID NO: 21	(gi 1709203)	61	QHFPSHKFI	120
SEQ ID NO: 22	(gi 1709205)		QRFPDSHKF	
SEQ ID NO: 2			KHYPDHKFI	
SEQ ID NO: 4			QLYPTHKFI	
SEQ ID NO: 6			MLYPDHKFI	
SEQ ID NO: 8				
SEQ ID NO: 21	(gi 1709203)	121	VGWVYDPII	180
SEQ ID NO: 22	(gi 1709205)		VGWVYNPII	
SEQ ID NO: 2			IGWVYNPII	
SEQ ID NO: 4			VGWVYNPII	
SEQ ID NO: 6				
SEQ ID NO: 8				
SEQ ID NO: 21	(gi 1709203)	181	INNLLFKVR	240
SEQ ID NO: 22	(gi 1709205)		INSLLFKVR	
SEQ ID NO: 2				
SEQ ID NO: 4				
SEQ ID NO: 6				
SEQ ID NO: 8				
SEQ ID NO: 21	(gi 1709203)	241	SGSEFDITS	277
SEQ ID NO: 22	(gi 1709205)		SGSEFDLT	
SEQ ID NO: 2				
SEQ ID NO: 4				
SEQ ID NO: 6				
SEQ ID NO: 8				

Figure 2A

```

1      1      2      3      4      5      6      7      8      9      10     11     12     13     14     15     16     17     18     19     20     21     22     23     24     25     26     27     28     29     30     31     32     33     34     35     36     37     38     39     40     41     42     43     44     45     46     47     48     49     50     51     52     53     54     55     56     57     58     59     60
SEQ ID NO:23 (gi 3915048) M-----TSAQKPVF-----SPSDLQT-----WL-----
SEQ ID NO:24 (gi 1652942) ML-----PEVEQRLF-----
SEQ ID NO:10 -----
SEQ ID NO:12 -----
SEQ ID NO:14 MLSSSSSTHSSTSPFPGLASANPNRRLRLRAAPVSSAVLSASGRQP-----MSTV
SEQ ID NO:16 -----
SEQ ID NO:18 MFSQCH-----FLSHSPIPNTT-FRLRAMAPHST-----
SEQ ID NO:20 -----HETKPSLP-----YHLRSPSLLATFSSSAAGRACGIAGRWMGSV

61      61      62      63      64      65      66      67      68      69      70      71      72      73      74      75      76      77      78      79      80      81      82      83      84      85      86      87      88      89      90      91      92      93      94      95      96      97      98      99      100     101     102     103     104     105     106     107     108     109     110     111     112     113     114     115     116     117     118     119     120
SEQ ID NO:23 (gi 3915048) -----EIA TEAVLAAGAEI--FSLWGKVVQIQEKGRAG
SEQ ID NO:24 (gi 1652942) -----IAQQLAAVSGEILIQYFRRSHLQGGTKIDQVS
SEQ ID NO:10 -----
SEQ ID NO:12 -----
SEQ ID NO:14 RASFAAGAAGRAAAVGE--LATERLVEVAQRAADAAGEVLRKYFRQ-RVEIIDKEDHSP
SEQ ID NO:16 -----
SEQ ID NO:18 -----PLELNRPAEVGNKVADAAGEVIRKYFRK-NFDVIHKHDLSP
SEQ ID NO:20 RAS-PSEAGGWAVAAAGKEGVDMERLVAVAQSAADAAGEVLRKYFRQ-RFEIIDKEDHSP

121     121     122     123     124     125     126     127     128     129     130     131     132     133     134     135     136     137     138     139     140     141     142     143     144     145     146     147     148     149     150     151     152     153     154     155     156     157     158     159     160     161     162     163     164     165     166     167     168     169     170     171     172     173     174     175     176     177     178     179     180
SEQ ID NO:23 (gi 3915048) DLVTEADRQAEAILLEIIKRRCPDHAILAEESG-QLGQVDNPPFCWAIDPLDGTTFNFAHSY
SEQ ID NO:24 (gi 1652942) AIVTQADEEAEQAMVDLIQAQFPQDGVIREEG--KNIAKSGYTWLDPIDGTSSSFVRGL
SEQ ID NO:10 -----HEDKLSSEVILEVTKNFRDHLILGEEGG-LIGDSLSEYLWCIDPLDGTTFNFAHY
SEQ ID NO:12 -----
SEQ ID NO:14 --VTIADREAEEMVSVILKSFPTHAIFGEENGWRCAESADFVWVLDPIDGTSKFITGK
SEQ ID NO:16 -----HE-----
SEQ ID NO:18 --VTIADQSAEEAMVSIILDNFPSHAIFYGEENGWRCBEKNADYVWVLDPIDGTSKFITGK
SEQ ID NO:20 --VTIADREAEEMTSVILKSFPTHAVFGEENGWRCAEKSAADYVWVLDPIDGTSKFITGK
```

Figure 2B

```

181                               240
SEQ ID NO:23 (gi 3915048) PVCSVIGLLIQDIPTGVVYNPFRQELFRAATSLGATLNR-----RPIQVSTTASLDK
SEQ ID NO:24 (gi 1652942) PIFATLIGLVADMRPVLGIAHQPISGDRWQVQEQESNVNGIP-LVNPYKASEINLTAA
SEQ ID NO:10 PSFSVIGVLYRGKPAATVVEFCGGPMCWSTRTISASSGKAYCNGQKIHVSPTEKVEQ
SEQ ID NO:12 -----MCWTTTRTFPPFAGGAYYIGQRIHVSQTDKVEQ
SEQ ID NO:14 PLFGTLIALLHNG-KPVIQVIDQPILRRERWIGVDGKQTTLNGQE-I--SVRSCNL-LAQA
SEQ ID NO:16 -----LTKVEQ
SEQ ID NO:18 PVFGTLVALLQNG-TPILGIIDQPVLRERWIGIAGKRTSLNGQE-I--STRTCAD-LSQA
SEQ ID NO:20 PLFGTLIALLHNG-KPVMGIIDQPILRERWVGVDGKTKTLNGQE-I--SVRPCNV-LEQA

241                               300
SEQ ID NO:23 (gi 3915048) SLLVTG---FAYDRVKTLDNNYPEFCYLTHLTQGVRRSGSAAIDLIDVACGRILDGYWERG
SEQ ID NO:24 (gi 1652942) CIVSTTPLMFTTPVQQQKMAIYRQCQRTAFGGDCFNLYLSAASGWTAMPLVIVEA----D
SEQ ID NO:10 SLLVTG---FGYEHDDAWLTNINLFKEFTDVSRRVRLGSAADMSHVGLGITEAYWEYR
SEQ ID NO:12 SLLVTGFGYEHDDAWTNNLNFKEFTDISRGVRR--LGSAAADMSHIGLITE---AYWE
SEQ ID NO:14 YLYTTSPLHFEADAEDA-FIRVRNKVKVPLYGCDVCYAYALLASGFVDI---VYES---G
SEQ ID NO:16 SLLVTG---FGYEHDDAWTNNLNFKEYTDISRGVRLGSAADMSHVALGITEAYWEYR
SEQ ID NO:18 YLYTTSPLHFNDAEEA-FIRVRSKVFKQLYGCDVCYAYALLSSGFVDL---VYES---G
SEQ ID NO:20 YLYTTSPLHFEADAEDA-FIRVRDKVKVPLYGCDVCYAYALLASGFVDL---VYES---G

301                               360
SEQ ID NO:23 (gi 3915048) INPWDMAAGIVIVREAGGIVSAVDCSPLDLSTGRILATNGKIHQELSQAALATPQ-----
SEQ ID NO:24 (gi 1652942) LNFYDFCALIPILTGANYCFTDWQKEL-----TPESTEVVASPNPKLHSE
SEQ ID NO:10 LKPWDMAGVLIIVEEAGGVVTRMDGGFTVFDRSVLVSNGVVDQLLERIRPATEDLKKK
SEQ ID NO:12 YRLKPWDVHAGVLIIVEEAGGVVTRMDGGFTVFDRSVLVSNGLVHGQV-----
SEQ ID NO:14 LKPYDFLSLVPVIEGAGGSITDWRGDKLH-----WPVTAESRPTSFNVVAAAGDARVHKE
SEQ ID NO:16 LKPWDMAGVLIIVEEAGGVVSRMDGGFTVFDRSVLVSNGVVDQLLDRIGPATEDLKKK
SEQ ID NO:18 LKPYDFLALIPVIEGAGGVITDWKGDKLF-----WEASPLSIATSFNVVAAAGDKQIHQQ
SEQ ID NO:20 LKPYDFLSLVPVIEGAGGSITDWEKNKLH-----WPVSSESERPTSFNVVAAAGDSHVHGQ

361                               381
SEQ ID NO:23 (gi 3915048) -----WF--QQYAAARAQKI
SEQ ID NO:24 (gi 1652942) ILAFL---Q-----
SEQ ID NO:10 GIDFSLWFKPKDKYPT---DF.
SEQ ID NO:12 -----CL
SEQ ID NO:14 ALDALRWR.-----
SEQ ID NO:16 GIDFSLWFKPKDKYPT---DF.
SEQ ID NO:18 ALDSLQWK.-----
SEQ ID NO:20 ALAALRWR.-----
```